Datos-Tomate

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```
library(tidyr)
dato <- data %>%
  gather(Variable, Valor, Hojas:Ancho)
head(dato)
```

Fecha	Tratamiento	Lote	Planta	Variable	Valor
<S3: POSIXct>	<chr>	<dbl>	<dbl>	<chr>	<dbl>
2023-09-22	T-C	1	17	Hojas	1
2023-09-22	T-C	1	17	Hojas	2
2023-09-22	T-C	1	17	Hojas	3
2023-09-22	T-C	1	17	Hojas	4
2023-09-22	T-C	1	17	Hojas	5
2023-09-22	T-C	1	17	Hojas	6

6 rows

Medidas de resumen por Varible de respuesta, fecha y Tratamiento

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```r
library(dplyr)
library(readxl)
library(dplyr)
library(agricolae)
library(moments)
library(ggplot2)
library(stringr)
dato %>%
  na.omit() %>%
  group_by(Variable, Tratamiento, Fecha) %>%
  summarise(
    "Mínimo" = min(Valor, na.rm = TRUE),
    "Máximo" = max(Valor, na.rm = TRUE),
    "Promedio" = mean(Valor, na.rm = TRUE),
    "Mediana" = median(Valor, na.rm = TRUE),
    "Desvío estándar" = sd(Valor, na.rm = TRUE),
    "CV" = (sd(Valor, na.rm = TRUE)/mean(Valor, na.rm = TRUE))*100,
    "Kurtosis" = kurtosis(Valor, na.rm = TRUE),
    "Asimetría" = skewness(Valor, na.rm = TRUE)
  )
```

```
`summarise()` has grouped output by 'Variable', 'Tratamiento'. You can override using the `.groups` argum
ent.
```

Variable <chr>	Tratamiento <chr>	Fecha <S3: POSIXct>	Mínimo <dbl>	Máximo <dbl>	Promedio <dbl>	Mediana <dbl>	Desvío estándar <dbl>	CV <dbl>
Ancho	T-B	2023-05-10	7.0	34.0	18.852113	18.00	7.214764	38.27032
Ancho	T-B	2023-09-22	3.5	24.0	12.113953	12.00	4.744148	39.16268
Ancho	T-B	2023-09-28	4.0	30.0	17.464000	17.00	7.507323	42.98742
Ancho	T-B	2023-10-02	2.0	45.0	20.261905	19.00	9.565085	47.20724
Ancho	T-B	2023-10-12	3.0	43.0	19.542169	19.00	9.618708	49.22027

Variable	Tratamiento	Fecha	Mínimo	Máximo	Promedio	Mediana	Desvío estándar	CV
<chr>	<chr>	<S3: POSIXct>	<dbl>	<dbl>	<dbl>	<dbl>	<dbl>	<dbl>
Ancho	T-B	2023-10-19	6.0	43.0	22.546218	22.00	9.449014	41.90953
Ancho	T-C	2023-05-10	4.0	38.0	16.981443	15.00	8.298598	48.86863
Ancho	T-C	2023-09-22	3.5	21.1	11.687234	11.00	5.027992	43.02123
Ancho	T-C	2023-09-28	7.0	30.0	19.083636	20.50	6.834546	35.81365
Ancho	T-C	2023-10-02	6.0	45.0	23.107759	23.00	8.388866	36.30324

1-10 of 54 rows | 1-9 of 11 columns   Previous **1** 2 3 4 5 6 Next
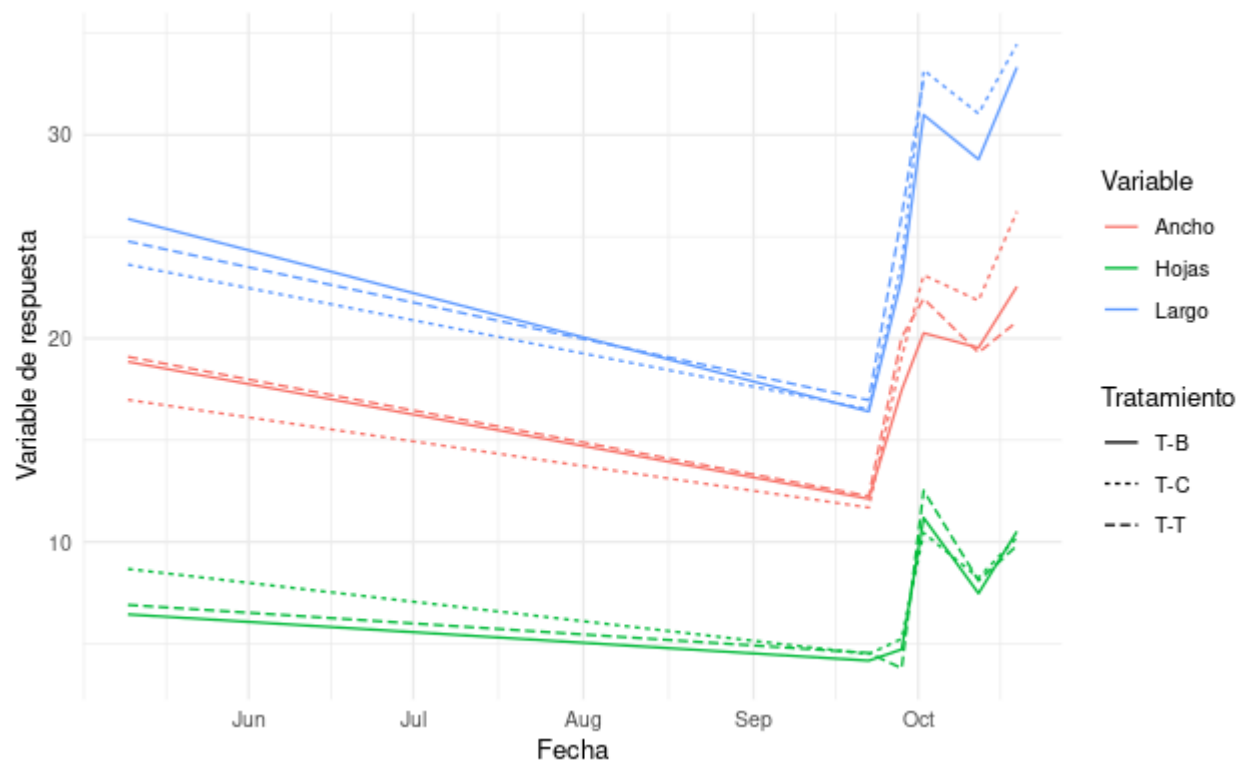
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```r
library(ggplot2)

promedio2 <- dato %>%
  group_by(Tratamiento, Variable, Fecha) %>%
  summarise(Valor = mean(Valor))
```

```
`summarise()` has grouped output by 'Tratamiento', 'Variable'. You can override using the `.groups` argument.
```

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```r
ggplot(promedio2, aes(x = Fecha, y = Valor, group = interaction(Tratamiento, Variable), color = Variable,
linetype = Tratamiento)) +
  geom_line() +
  labs(x = "Fecha", y = "Variable de respuesta") +
  theme_minimal()
```

# Filtrado para última fecha ya que todas la mediciones de fechas anteriores son dependientes

```
datos <- data %>%
    filter(Fecha == max(Fecha))
```
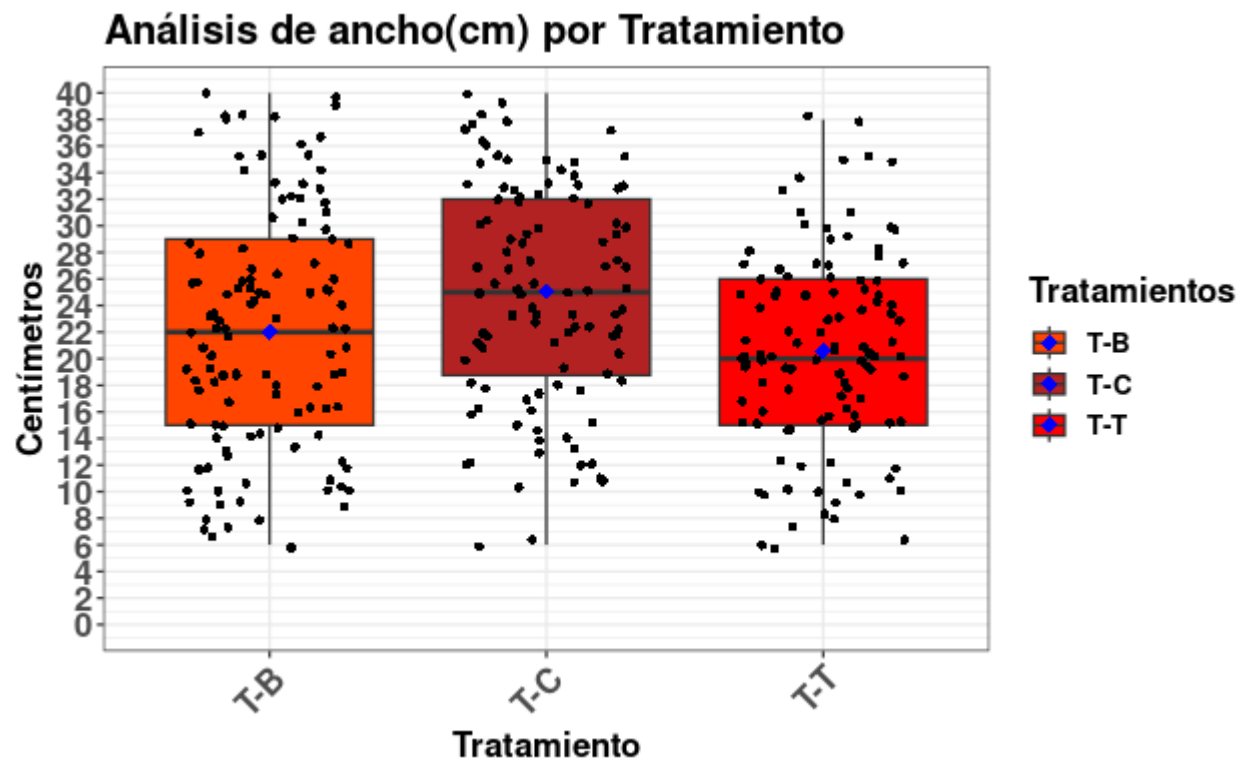
Boxtplot de hojas

```
ggplot(datos, aes(x = Tratamiento, y = Hojas, fill = Tratamiento)) +
  geom_boxplot() +
  geom_jitter(shape = 16, position = position_jitter(0.3)) +
  stat_summary(fun = mean, geom = "point", shape = 18, size = 3, color = "red") +
  scale_y_continuous(limits = c(0, 25), breaks = seq(0, 25, by = 2)) +
  labs(y = "Cantidad de hojas", x = "Tratamiento", fill = "Tratamientos", title = "Análisis de Hojas por
Tratamiento") +
  theme_bw() +
  theme(
    text = element_text(size = 14, face = "bold"),
    axis.text.y = element_text(size = 14),
    axis.text.x = element_text(size = 14, angle = 45, hjust = 1)  # Añadido para inclinar las etiquetas e
n el eje x
  ) +
  scale_fill_manual(values = c("T-B" = "#458B00", "T-C" = "#556B2F", "T-T" = "#CDAD00"))
```

Análisis de Hojas por Tratamiento
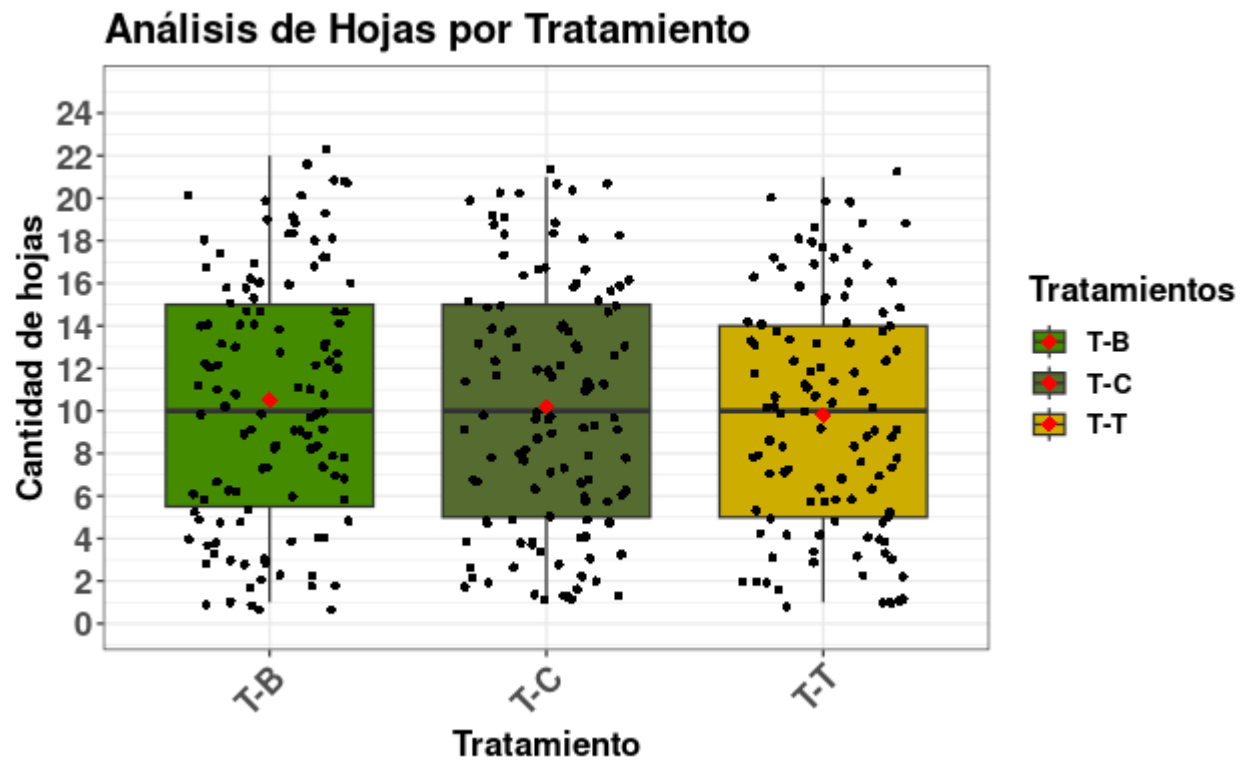
# Boxtplot de Ancho

Hide

```
ggplot(datos, aes(x = Tratamiento, y = Ancho, fill = Tratamiento)) +
  geom_boxplot() +
  geom_jitter(shape = 16, position = position_jitter(0.3)) +
  stat_summary(fun = mean, geom = "point", shape = 18, size = 3, color = "blue") +
  scale_y_continuous(limits = c(0, 40), breaks = seq(0, 40, by = 2)) +
  labs(y = "Centímetros", x = "Tratamiento", fill = "Tratamientos", title = "Análisis de ancho(cm) por Tr
atamiento") +
  theme_bw() +
  theme(
    text = element_text(size = 14, face = "bold"),
    axis.text.y = element_text(size = 14),
    axis.text.x = element_text(size = 14, angle = 45, hjust = 1)
  ) +
  scale_fill_manual(values = c("T-B" = "#FF4500", "T-C" = "#B22222", "T-T" = "#FF0000"))
```


Análisis de ancho(cm) por Tratamiento

Boxtplot de Largo

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```
ggplot(datos, aes(x = Tratamiento, y = Largo, fill = Tratamiento)) +
  geom_boxplot() +
  geom_jitter(shape = 16, position = position_jitter(0.3)) +
  stat_summary(fun = mean, geom = "point", shape = 18, size = 3, color = "red") +
  scale_y_continuous(limits = c(9, 50), breaks = seq(9, 50, by = 2)) +
  labs(y = "Centímetros", x = "Tratamiento", fill = "Tratamientos", title = "Análisis de largo(cm) por Tr
atamiento") +
  theme_bw() +
  theme(
    text = element_text(size = 14, face = "bold"),
    axis.text.y = element_text(size = 14),
    axis.text.x = element_text(size = 14, angle = 45, hjust = 1)
  ) +
  scale_fill_manual(values = c("T-B" = "#87CEFA", "T-C" = "#BBFFFF", "T-T" = "#90EE90"))
```

Análisis de largo(cm) por Tratamiento
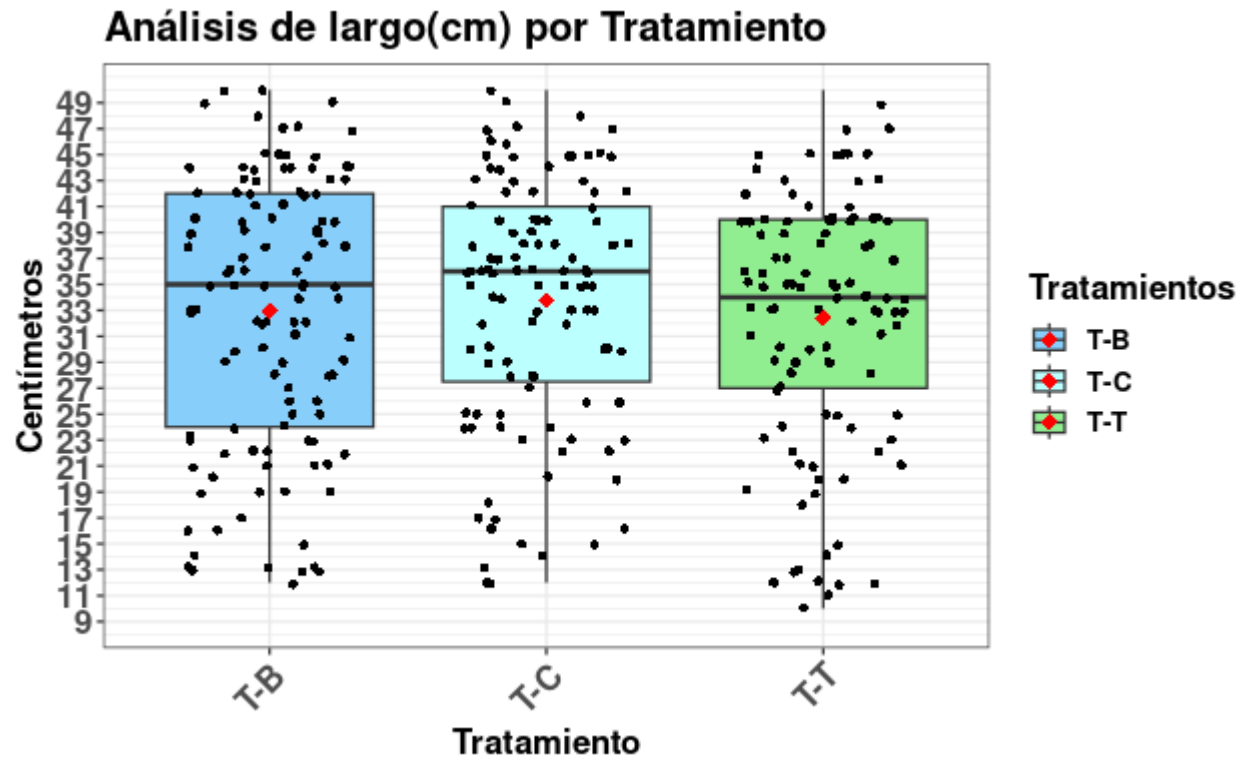
Annova de hojas

Hide

```
modelo = aov(Hojas ~ Tratamiento, data = datos)
summary(modelo)
```

```
            Df Sum Sq Mean Sq F value Pr(>F)
Tratamiento   2     28   13.84   0.419  0.658
Residuals   341  11260   33.02
```

No presenta diferencias significativas

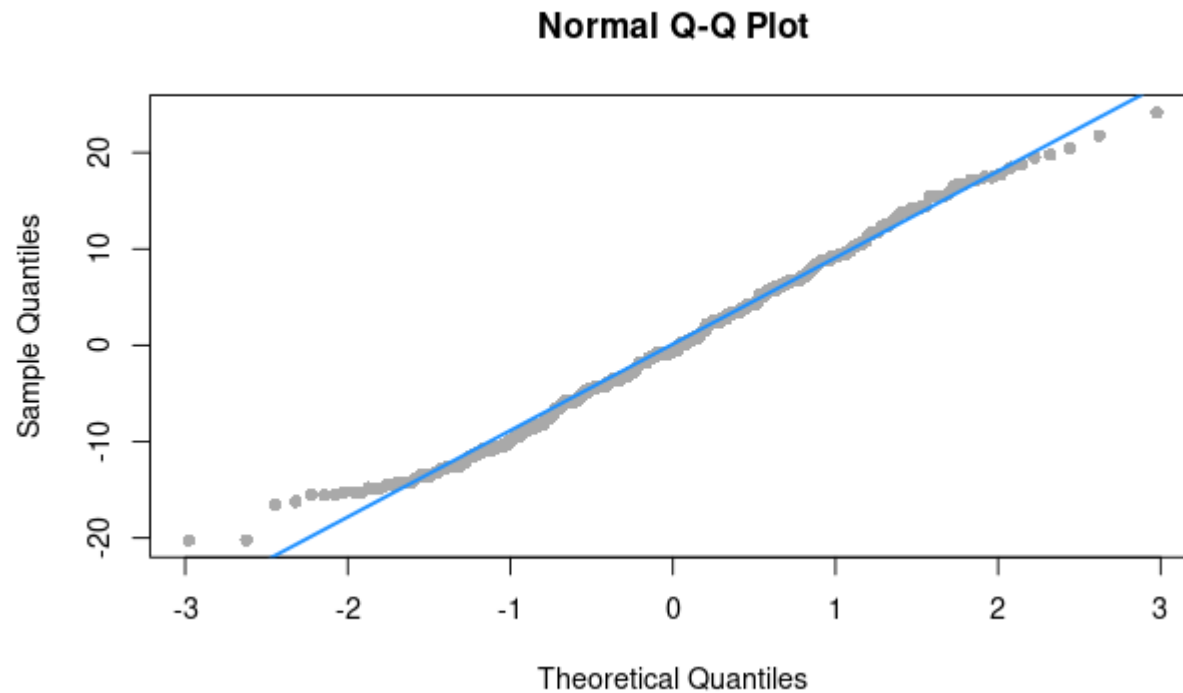# Annova de Ancho

```
modelo = aov(Ancho ~ Tratamiento, data = datos)
summary(modelo)
```

```
             Df Sum Sq Mean Sq F value   Pr(>F)
Tratamiento   2   1734   866.9   10.91 2.55e-05 ***
Residuals   341  27087    79.4
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Pruebas de normalidad

```
qqnorm(modelo$residuals,pch=16,col = "darkgrey")
qqline(modelo$residuals, col = "dodgerblue", lwd = 2)
```

Normal Q-Q Plot

Los errores se distribuyen normal de manera gráfica

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```
shapiro.test(modelo$residuals)
```
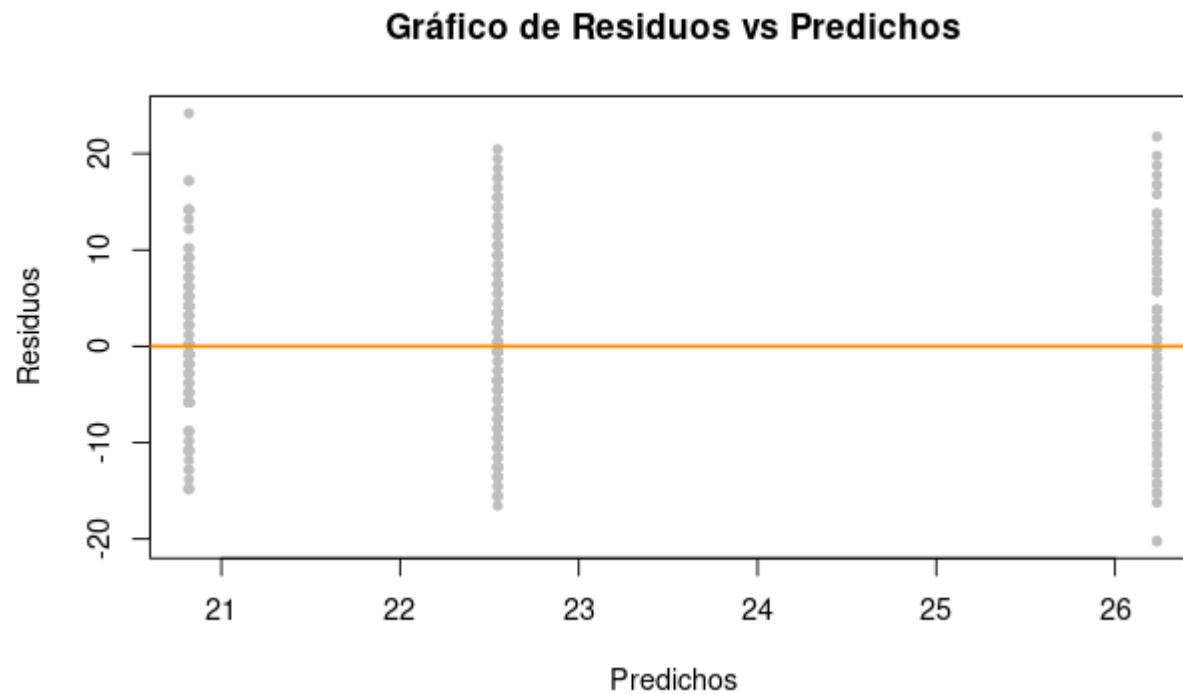
```
    Shapiro-Wilk normality test

data:  modelo$residuals
W = 0.98975, p-value = 0.01645
```

los errores se distribuyen normal

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```
plot(modelo$fitted.values,
modelo$residuals,
col = "grey",
pch = 20,
xlab = "Predichos",
ylab = "Residuos",
main = "Gráfico de Residuos vs Predichos")
abline(h = 0, col = "darkorange", lwd = 2)
```

Gráfico de Residuos vs Predichos

Las varianzas son homogéneas.

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```
library(lsmeans)
```

```
Loading required package: emmeans
The 'lsmeans' package is now basically a front end for 'emmeans'.
Users are encouraged to switch the rest of the way.
See help('transition') for more information, including how to
convert old 'lsmeans' objects and scripts to work with 'emmeans'.
```

Hide

```
marginal = lsmeans(modelo, ~ Tratamiento)
```

Hide

```
library(agricolae)
library(multcomp)
CLD = cld(marginal,
  alpha = 0.05,
  Letters = letters,
  adjust = "tukey")
```

```
Note: adjust = "tukey" was changed to "sidak"
because "tukey" is only appropriate for one set of pairwise comparisons
```

Hide

```
print(CLD)
```

```
 Tratamiento lsmean    SE  df lower.CL upper.CL .group
 T-T            20.8 0.850 341     18.8     22.9  a
 T-B            22.5 0.817 341     20.6     24.5  a
 T-C            26.2 0.831 341     24.2     28.2   b


Confidence level used: 0.95
Conf-level adjustment: sidak method for 3 estimates
P value adjustment: tukey method for comparing a family of 3 estimates
significance level used: alpha = 0.05
NOTE: If two or more means share the same grouping symbol,
      then we cannot show them to be different.
      But we also did not show them to be the same.
```
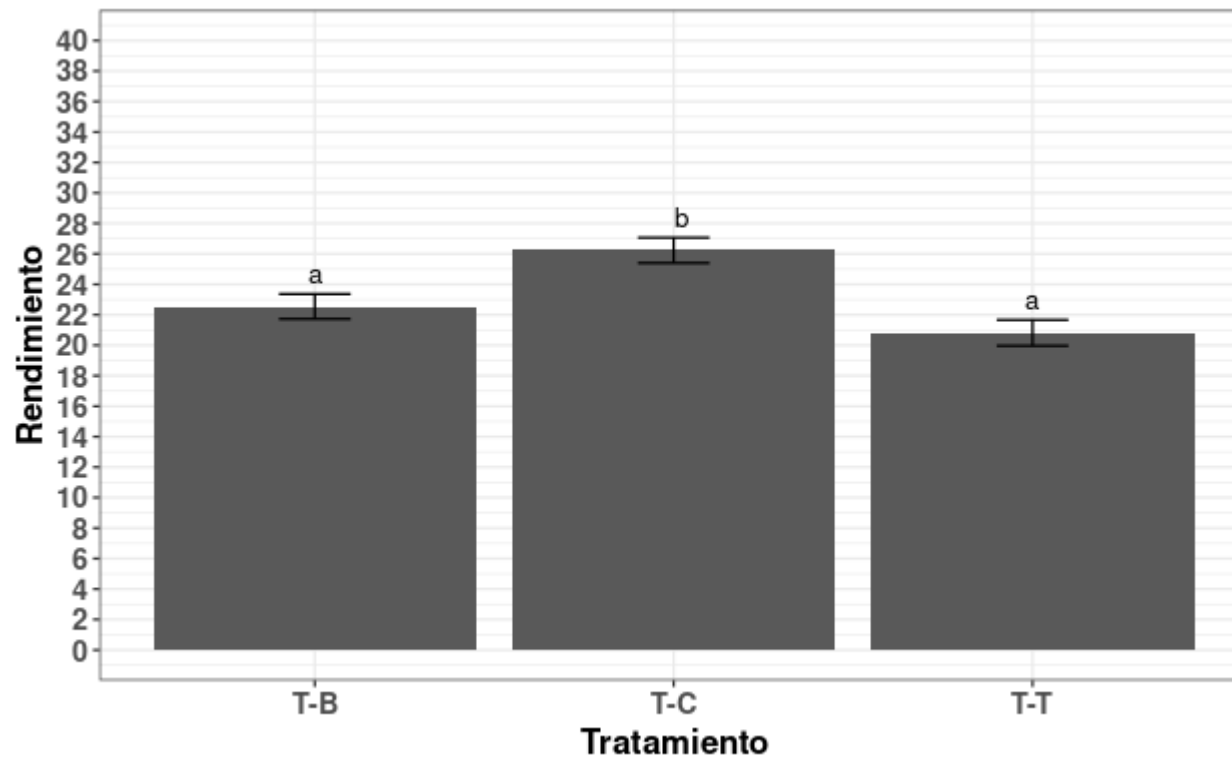
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```
ggplot(CLD,aes(x=Tratamiento,y=lsmean))+
  geom_bar(stat = "identity")+
  geom_errorbar(aes(ymin=lsmean-SE, ymax=lsmean+SE),

  width=0.2,
  position=position_dodge(1))+

  geom_text(aes(y = lsmean + SE,
  x = Tratamiento,
  label = .group),hjust = 0.5,vjust = -0.5)+

  scale_y_continuous(limits = c(0,40),breaks = seq(0, 40, by = 2))+
  labs(y="Rendimiento",legend="Variedad")+
  theme_bw()+
  theme(
  text = element_text(size = 14, face = "bold"),
  axis.text.y = element_text(size = 12),
  axis.text.x = element_text(size = 12))
```

Annova de Ancho

Hide

```
modelo = aov(Largo ~ Tratamiento, data = datos)
summary(modelo)
```

```
            Df Sum Sq Mean Sq F value Pr(>F)
Tratamiento   2    192   95.79   0.912  0.403
Residuals   341  35812  105.02
```

La variable largo no tiene diferencias significativas

Correlaciones de pearson en las variables de respuesta

```
frame <- na.omit(frame)
library(corrplot)
  corrplot.mixed(cor(frame),
  lower = "number",
  upper = "circle",
  tl.col = "black")
```